Using stand conditions, latitude, elevation, and allometric relationships to model coastal Douglas-fir crown biomass

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Abstract

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Modern forest management goals require highly accurate measurement of more sophisticated forest metrics than those that were used in the past. This study aims to explore more accurate techniques for measuring crown (and crown component) biomass for coastal Douglas-fir trees. Although methods for estimating such metrics for Douglas-fir exist, many of these methods lack accuracy and very few, if any, even begin to account for relevant environmental information. In order to accomplish the aforementioned goals, 16 Douglas-fir trees were sampled in the Pacific Northwest using an orthogonal experimental design (accounting for stand density, latitude and social position) and combined to another data set of 30 destructively sampled Douglas-fir trees from Southwest Washington State. All sample trees were from planted, industrially managed forestland. Subsequent analysis produced five different component-specific equations for: [1] total live crown biomass, [2] total live branch biomass, [3] total foliar biomass, [4] total dead branch biomass, and [5] total (live and dead) crown biomass. Model accuracies range from 67% - 84% (1 – [MAE/mean component biomass]). A subset of these models ([1], [2], [3]) were then validated using a fully independent dataset of 32 Douglas-fir trees collected on a naturally regenerated Douglas-fir stand in Southwest Oregon with accuracies of 69% - 83%.

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INTRODUCTION

Allometric equations generated from empirical data are often used to estimate tree and forest biomass. These equations are typically species-specific, and are frequently calculated in sets that allow for component itemization of biomass estimates. Examples of component groups include, but are not limited to: foliage, live branch, dead branch, bark, bole, and whole-tree. The uses for these biomass estimation methods are multi-faceted. In studies like that of Ares et al. (2007), researchers can use biomass component estimates to examine the impacts of forest operations on nutrient cycling. Bradshaw et al (2015) and others (Anderson et al. 2011) have demonstrated that these equations can also be coupled with remote sensing data to quantify forest and landscape-level carbon sequestration. These techniques also have a clear place in applied forestry and forest operations, as land managers can use allometric biomass equations to calculate pre-harvest slash estimates and assess biofuel energy feedstocks.

Although multiple studies have deduced biomass models for Douglas-fir in the Pacific Northwest of the United States, few have begun to characterize the role that stand conditions and over-arching environmental influences play in determining variation in component biomass allocation, even though previous research and general forestry concepts suggest the presence of such influences. In Douglas-fir trees, there are indications that much of this variation is exhibited in the crown. Coastal Douglas-fir crown research by Hann (1997) indicates the potential effect of latitude on crown characteristics in that separate coefficients were needed to describe populations in Northwest and Southwest Oregon and unpublished work by Turnblom et al. (2015) found similar indications in coastal Western hemlock populations of Washington State. Stand density also appears to play a role in crown biomass allocation. Work by Harry et. al. (1964) describes an observed decrease in Douglas-fir crown widths in trees that grew in more dense stands.

The objective of this study is to use data from destructively sampled coastal Douglas-fir trees from stands throughout Western Washington and Western Oregon to help explore and model the influence of environmental and stand conditions on Douglas-fir crown characteristics. Variables of particular interest are: stand density, latitude and stand social position.

METHODS

2.1 STUDY AREA

This study was conducted in Western Washington and Northwestern Oregon within the latitude range of 43.92330 N to 48.50128 N degrees and longitude range of 123.6086 W to 121.6281 W degrees. Elevations range from 572ft to 2200ft above sea level. *Table 1* summarizes sampling location information. All samples were collected on public and private industrially managed forestland. *Figure 1* illustrates the spatial arrangement of study sites.

Figure 1) location of study sites from North to South, these points represent Sauk Mountain (Inst. 713), Kitten Knob (Inst. 711), Fall River, Silver Creek Mainline (Inst. 722), and Trail Creek (Inst. 710).

2.2 EXPERIMENTAL DESIGN

Biometric measurements for this analysis come from 46 destructively sampled Douglas-fir trees taken from locations described above. Within this dataset, 16 trees are from a biomass study implemented by researchers at the University of Washington (these trees will be referred to hereafter as the UW dataset). Sampling protocol for the UW trees adhered to a balanced, fully-crossed experimental design focusing on the following variables: stand age, stand density, social position (crown competition) and geography (latitude). Only the "young" portion of the UW trees were available for this analysis, so all of these samples are between 39 and 40 years old. Stand density selection was based on Curtis's relative density (1982), which is calculated using a stand's quadratic mean DBH (diameter at breast height) and stand basal area. Low density stands had relative densities in the 30's and 40's while high density stands had relative densities in excess of 57. Competitive position was determined using diameter distribution. Half of the UW samples are dubbed intermediate trees and come from the third quintile (40th – 60th percentile) of a stand's DBH distribution while the other half are dubbed dominants and come from the fifth quintile (80th – 100th percentile). The latitude of 46.599 N serves as the distinction between Northern and Southern stands in this dataset, this line falls close to Chehalis, Washington. Half of the UW stands come from well north of this line while the other half come from well south of it. All of the UW trees come from pure, planted Douglas-fir stands on industrial managed lands.

The remaining 30 trees used for model building in this analysis come from the work of Harrison et al. (2009) (Hereafter referred to as the Fall River or FR dataset). These trees were collected as part of a larger project to assess site productivity and characteristics on industrial forest land before and after harvest. Biomass trees were selected to be proportionally representative of diameter and height class distributions generated from the entire study area. It is important to note that although the Fall River trees were also planted, and come from industrially managed forestland, the site experienced significant western hemlock ingrowth. At the time of biomass sampling, 52.7% of the trees on site were western hemlock by count, but the planted Douglas-fir were still larger on average (mean DBH of 14.9 in vs. western hemlock's 13.08 in), meaning that more of Fall River's total basal area (53.6%) was still comprised of Douglas-fir.

2.3 FIELD METHODS

For the UW trees, once a pool of candidate stands was determined using the previously mentioned qualifying characteristics (latitude, relative density and age), an adequate subset was randomly selected and field checked for feasibility. If suitable, trees in the selected stand would then be measured for DBH and sample trees were randomly selected within their distribution quintile to yield one dominant tree and one intermediate tree per stand. Trees were determined to be unsuitable for sampling if they exhibited abnormal growth characteristics (crown or bole damage, forked-top, disease, etc...). Before felling, each sample tree was marked horizontally at 1 ft (stump), 2.75 ft (half way to breast height), and 4.5 ft (breast height) and a vertical line was drawn along the due-North azimuth of the stem. The tree was then felled into as clear an alley a possible. On the ground, the tree was marked at ten-foot intervals up to a four-inch stem diameter. Total tree height was recorded as well as height to the live-crown-base. Length of the top section above the four-inch stem diameter was measured at this time in addition to the following height measurements: lowest live branch, lowest dead branch and highest dead branch. The distance between the highest and lowest dead branches was used to define an area of occurrence for dead branches on each tree. A dead sample branch was randomly selected within each third of this portion of the tree to yield a total of three dead sample branches. A similar method was used to select three living sample branches from the tree’s live-crown. All sample branches were then weighed in the field, bagged, and brought back to the lab for further analysis. All remaining branches were removed from the stem at each ten-foot interval and weighed, with live and dead branches weighed separately. Two-inch thick disks were cut from a tree’s stem at the 1 ft stump, 2.75 ft, 4.5 ft, and at 10-ft intervals running up the tree, up to, and including, the stem’s 4-inch diameter. The tree’s top (above stem’s 4-inch diameter section) was separated into branches and stem and weighed separately.

Data from the Fall River (FR) trees was collected in a similar fashion. As previously described, sample trees were selected to be proportionally representative of the study area’s species-specific diameter and height distributions. Total tree height and height to live-crown-base were measured after felling. For all sample trees, dead and live branches were weighed separately and a representative sample of live and dead branches were taken back to the University of Washington lab facilities for further analysis after wet wets were assigned in the field. Eight disks of 10-cm thickness were cut from log sections, in addition to one disk from the tree’s 5 cm diameter section. These were also taken back to the lab for analysis.

Table 1) *Summary information for sampling plots and sample trees used as the modeling data for this analysis.*

Plot Data							**Sample Trees**						
Location	**Trees (N=)**	**Latitude**	**Elevation (ft)**	**Relative Density Range**	**QMD Range (in)**	**Age**	**Min. DBH (in)**	**Mean. DBH (in)**	**Max. DBH (in)**	**Min. Height (ft)**	**Mean Height (ft)**	**Max. Height (ft)**	**Live Crown Ratio Range (%)**
Inst. 710	4	43.92 N	600	39 - 55	10.3 - 14.1	40	10.1	13.8	18.1	92.5	102	109.5	33.7 - 37.1
Inst. 711	4	48.32 N	572	36 - 68	11.4 - 14.9	39	10.5	14.4	18.6	101.5	104.3	110	38.7 - 51.2
Inst. 713	4	48.50 N	793	32 - 62	9.3 - 12.7	40	8.7	11.1	13.9	75	89	113.5	37.7 - 53.9
Inst. 722	4	44.88 N	2200	47 - 62	11.4 - 16.9	40	10.6	15.3	19.4	88.2	93.1	99.9	35.2 - 51.6
Fall River	30	46.72 N	1094	42 - 51	13.7 - 16.1	47	5.9	18.5	31.5	77.4	113.7	130.6	20.7 - 55.9

2.4 LAB METHODS

Sample branches from both the FR and UW datasets were dried in an oven to a constant weight; the only difference being that FR branches were dried at 65 degrees C while UW trees were dried at 100 degrees C. Dry branch weights were used to generate wet:dry ratios and needles were separated from branches to generate branch:foliage ratios. These ratios were applied to field measurements at corresponding heights to determine total dry branch and foliar weight estimates. For the UW trees, wet volumes were determined for log disks by way of eight radial measurements taken from the top and bottom of each disk, as well as eight width measurements. After wet volumes were assigned, the log disks were dried at 100 degrees C to a stable weight and separate dry weights were determined for bark and bole material. These volume measurements and oven-dry weights were then used to generate total bark and bole biomass estimates for each tree, as well as specific gravity.

For the FR log-disks, green volumes were determined through four perpendicular bark thickness measurements, two inside-bark diameter measurements and three disk thickness measurements. Disks were then dried at 65 degrees C to a constant weight and separate dry weights were determined for bark and bole. These metrics were then used to determine bark and bole biomass estimates for the rest of the tree’s stem.

The present analysis focuses on branch, foliage, and crown biomass. Bark and bole components will be reported in a separate document.

2.5 DATA

Measurements from the UW and FR trees, along with corresponding plot information were combined to form a single dataset of 46 observations and subsequently used to produce the component biomass models of this study. The modeling dataset includes three categories of predictor variables: tree (e.g. DBH, HT, BAL, LCR, DBH.perc, QMD.ratio, HT.ratio), stand (e.g. TPA, BAA, RD), and environmental (Lat, Elev). *Table 2* summarizes the twelve predictor variables used in this analysis.

Table 2) Pool of predictor variables for component biomass modeling

Model Term	**Description**	**Min**	**Mean**	**Max**
DBH	Stem diameter at 4.5 ft (in)	5.9	16.8	31.5
HT	Tree height (ft)	75	108	130.6
LCR	Ratio of: Live crown length / Tree height (%)	20.7	41.5	55.9
BAA	Plot basal area per acre (ft^2)	115	252.7	318.7
BAL	Sum of plot basal area for trees larger than sample (ft^2)	0	74.61	288.4
TPA	Trees per acre	116	240	402
DBH.perc	DBH percentile (%)	1.1	69.4	100
RD	Curtis's (1982) Relative Density	32.2	48.8	68.2
Elev	Elevation (ft)	572	1075	2200
Lat	Latitude (decimal degrees)	43.9	46.6	48.5
QMD.ratio	Ratio of: sample DBH / plot quadratic mean DBH	0.4	1.1	2.01
HT.ratio	Ratio of: sample height / plot mean height	0.75	1.06	1.35

A third independent validation dataset (N=32) was also used in this analysis. These Douglas-fir trees were sampled by USFS researchers, Nay and Bormann (2007), on a 0.5-hectare plot in the Siskiyu Mountains of Southwest Oregon (hereafter referred to as the SISK dataset). It should be mentioned that there are a few prominent differences between the stands used for modeling and the study sites of Nay and Bormann. The SISK study area is much further south (43.36 N) and was naturally regenerated after a fire. Because of this, the stand is Douglas-fir-dominated, but also multi-aged and mixed-species with dominant ages generally ranging from 70 – 100 years and a second-story consisting of mixed hardwoods like tanoak, Pacific madrone and golden chinkapin. Data collection methods also differ in that sampling was not completely destructive. Instead, sample trees were climbed and crown components were estimated through branch diameter measurement and stratified sub-sampling (15 branches per tree).

2.6 MODELING

The component biomass models produced in this analysis were developed using both backward and forward stepwise ANOVA regression (alpha of .05), automated regression (using R's MASS package, version 7.3-47), assessment of residuals, and predictive performance on an unincorporated and completely independent dataset. It should be mentioned that automated regression was never used as a stand-alone method for term selection, but instead, was used to double-check the results of manual stepwise regression. Residuals were scrutinized throughout the term selection process and a variety of diagnostic and visualization techniques were employed. Examples of visualization techniques include: prediction-vs-residual plots for examining normality and heteroscedasticity in potential final models (*Figure 2*) and variable-vs-residual plots for justifying term addition in forward stepwise regression. Examples of non-visual residual assessment techniques include: the Breusch-Pagan (1979) non-constant variance score test for further examining heteroscedasticity and Cook's (1979) distances for assessing influential outliers. Because a number of these metrics have the potential to be highly correlated, multicollinearity was closely monitored throughout model reduction using variance inflation factor (VIF). For all component models, a box-cox transformation indicated that natural-log-transformation of the response variable would improve normality.

For each biomass component, the reduced models resulting from forward, backward and automated regression were compared. If the models included different terms from one another, additional stepwise regression and investigation was applied until a satisfactory base model was produced. A Box-Tidwell transformation was then applied to determine the suitability of any predictor variable transformations and second-order interaction terms were assessed.

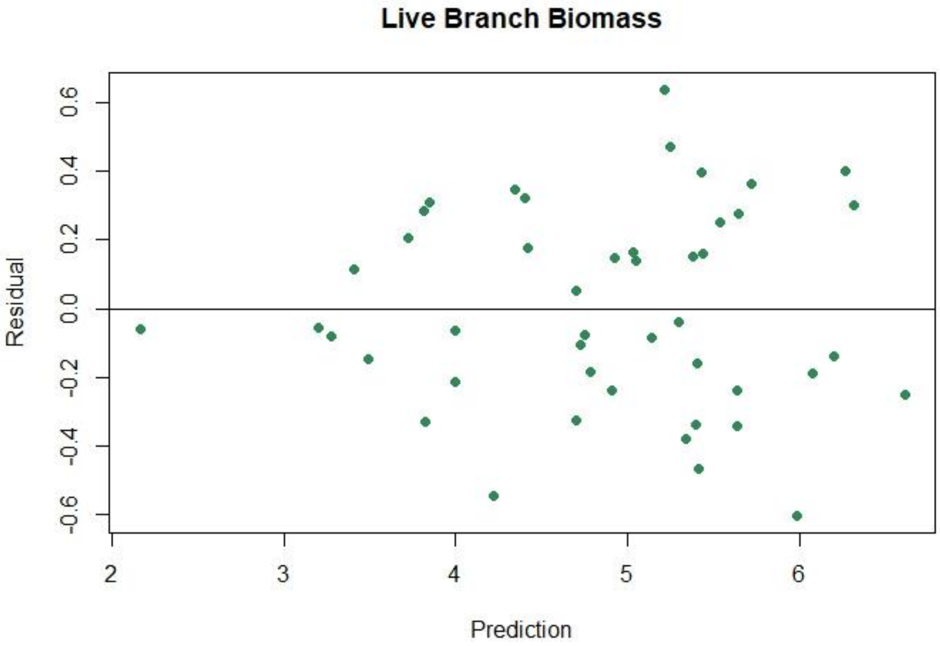

Figure 2) Example of reasonable stundentized residual vs prediction plot. These types of plots were used to assess every component biomass model.

RESULTS

3.1 TOTAL LIVE CROWN

The final model for estimating total live crown biomass (sum of all living branches, foliage and branch bark) can be expressed as:

$$\mathbf{[1]\ ln(LC)} = \underset{(0.311)}{-1.8172} + \underset{(0.137)}{2.4151}\mathbf{ln}(\mathbf{DBH}) + \underset{(0.006)}{0.0171}\mathbf{LCR} - \underset{(0.0007)}{0.0015}\mathbf{BAA}$$

Where LC is live crown biomass in dry pounds, and predictor variables are the same values described in *Table 4*. This model's back-transformed pseudo-R-squared (1 – [back-transformed SSE / SST]) was 0.856, its root mean squared error (RMSE) was 78.5 dry lbs and its mean absolute error (MAE) was 52.6 dry-pounds (21.1% of mean total live crown biomass). On average, the equation slightly underestimates live crown biomass with a mean bias of -6.49 lbs. Natural log transformation of DBH improved model normality and performance. No second order interaction terms improved model performance. *Figure 3* illustrates model performance and comparison of predicted and observed total live crown values for the modeling dataset (FR and UW). *Table 3* summarizes model performance metrics for all biomass models. Standard errors are reported beneath each coefficient.

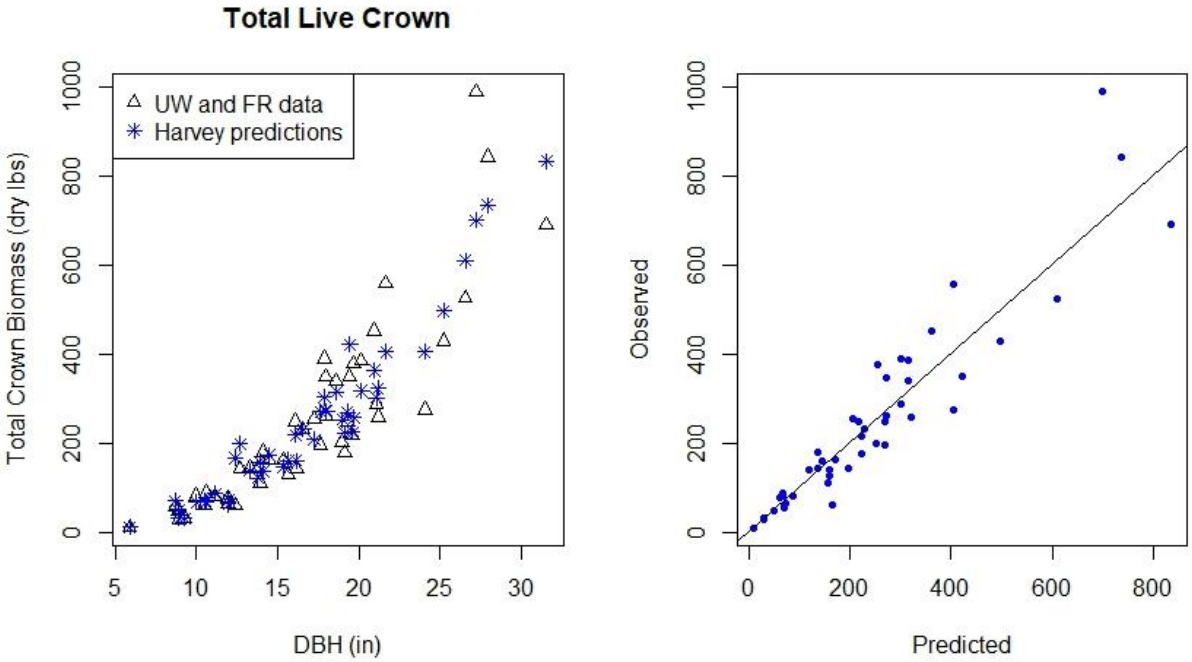

Figure 3) Predictions for total live crown biomass (blue) against observed values from the FR and UW trees

3.2 LIVE BRANCH

The final model for estimating live branch biomass (includes branch bark, but no foliage) can be expressed as:

[2] ln(LB) = 2.0552 + 0.0964*ln(**DBH)** + 0.0304***LCR** – 0.0149***RD** + 0.0099***DBH.perc**

(0.4102) (0.0135) (0.0062) (0.0059) (0.0027)

Where LB is live branch biomass in pounds. This model's back-transformed pseudo-R-squared was 0.877, its RMSE was 62.11 dry lbs, and its MAE was 43.16 dry lbs (21.9% of mean live branch biomass). The equation slightly under predicts, with a mean bias of -1.72 lbs. Transformations of predictor variables did not improve performance, nor did any second order interaction terms. *Figure 4* illustrates model performance and comparison of predicted and observed live branch biomass values for the modeling dataset (FR and UW). Standard errors are reported beneath each coefficient.

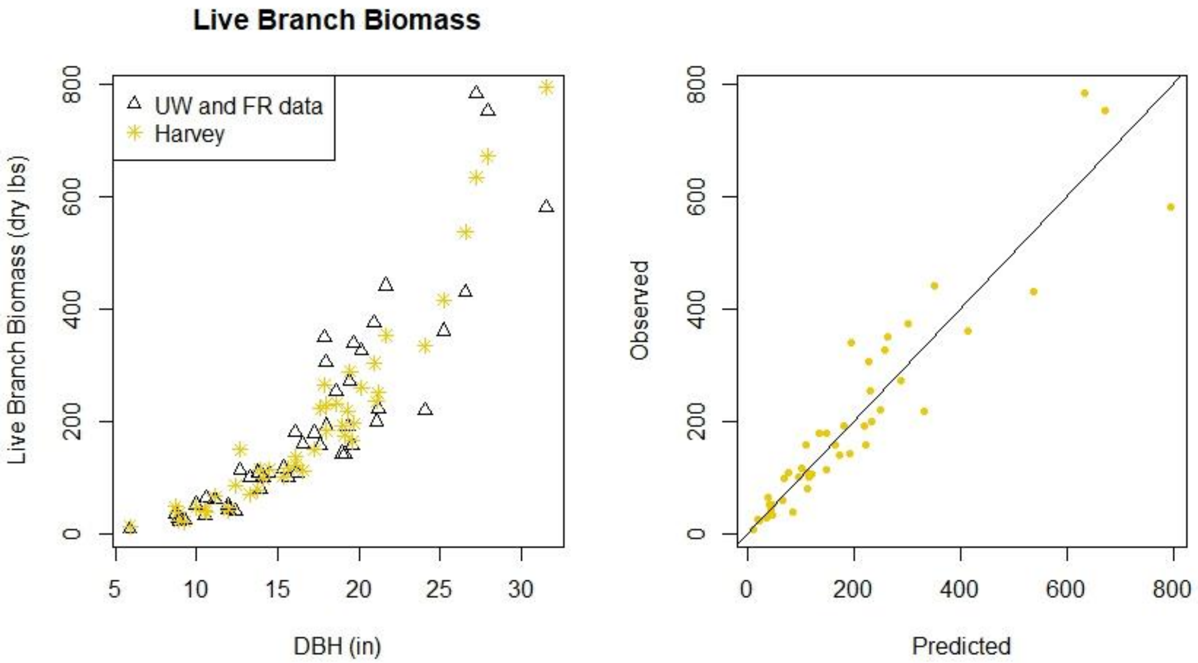

Figure 4) Predictions for live branch biomass (yellow) against observed values from the FR and UW trees

3.3 FOLIAGE

The final model for estimating foliar biomass can be expressed as:

$$\textbf{[3] ln(FOL)} = \underset{(0.6779)}{-4.0777} + \underset{(0.2527)}{3.5723}\textbf{DBH}^{1/3} - \underset{(0.0010)}{0.0010}\textbf{BAA} + \underset{(0.0074)}{0.0200}\textbf{RD}$$

Where FOL is live branch biomass in pounds. This model's back-transformed pseudo-R-squared was 0.568, its RMSE was 23.43 dry lbs, and its MAE was 14.67 dry lbs (27.9% of mean foliage biomass). The equation slightly under predicts, with a mean bias of -0.4 lbs. A Box-Tidwell transformation of predictor variables indicated that a cube root transformation of DBH would improve model normality. No second order interactions improved model performance. *Figure 5* illustrates model performance and comparison of predicted and observed foliage biomass values for the modeling dataset (FR and UW). Standard errors are reported beneath each coefficient.

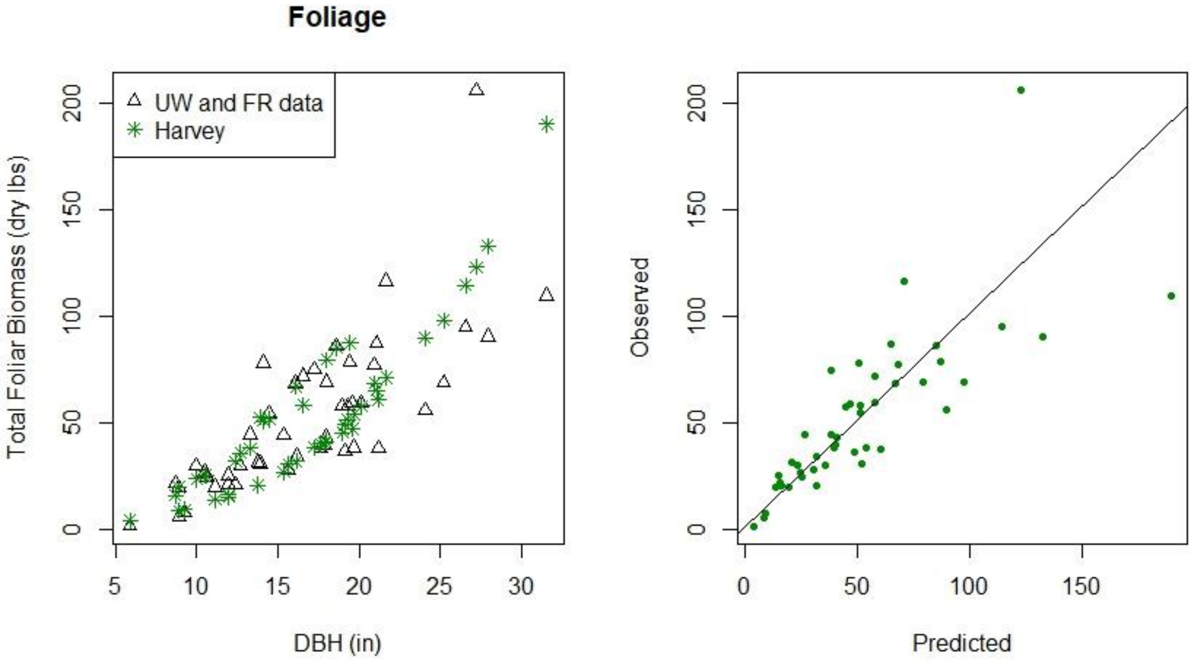

Figure 5) Predictions for total foliar biomass (green) against observed values from the FR and UW trees

3.4 DEAD BRANCHES

The final model for estimating dead branch biomass can be expressed as:

$$\mathbf{[4]\ ln(DB)} = \underset{(0.482)}{2.8644} + \underset{(0.029)}{0.1039}\,\mathbf{DBH} - \underset{(0.0014)}{0.0044}\,\mathbf{TPA} + \underset{(0.0055)}{0.0097}\,\mathbf{DBH.perc}$$

Where DB is dead branch biomass in pounds. This model's back-transformed pseudo-R-squared was 0.69, its RMSE was 53.95 dry lbs, and its MAE was 35.60 dry lbs (33.7% of mean dead branch biomass). The equation under predicts, with a mean bias of -7.61 lbs. Transformations of predictor variables did not improve performance. The interaction between DBH and DBH percentile was significant, but did not improve model performance. *Figure 6* illustrates model performance and comparison of predicted and observed dead branch biomass values for the modeling dataset (FR and UW). Standard errors are reported beneath each coefficient.

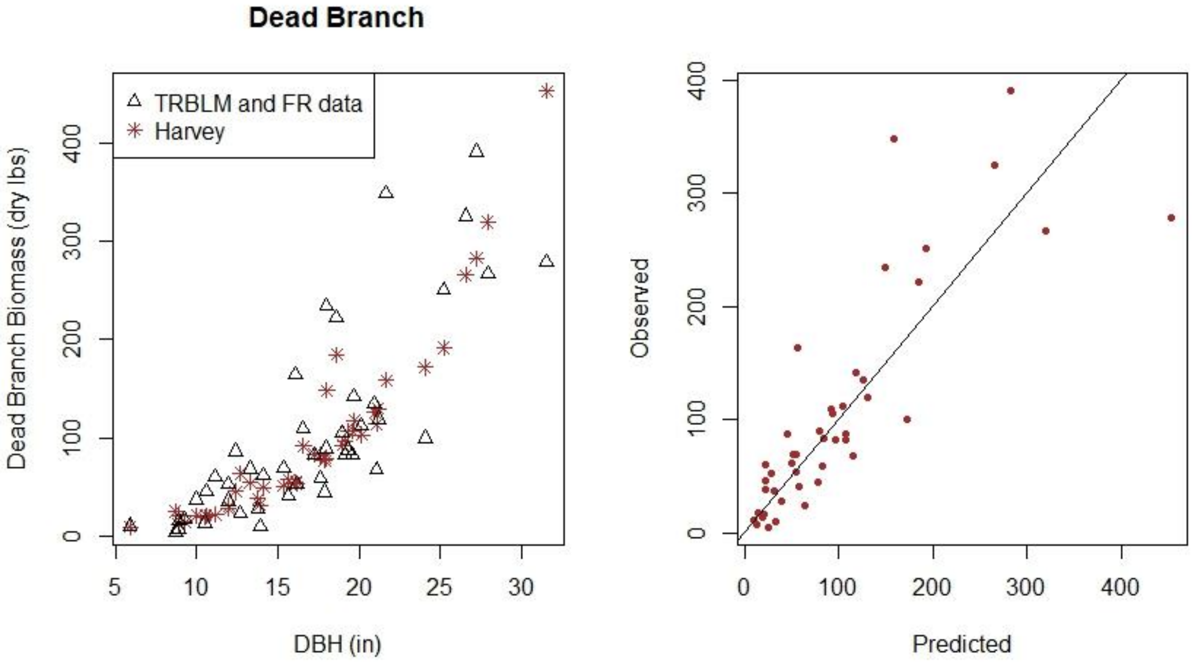

Figure 6) Predictions for total dead branch biomass (brown) against observed values from the FR and UW trees

3.5 TOTAL CROWN

The final model for estimating total crown (all living and dead crown components) can be expressed as:

[5]
$$\ln(\mathbf{TC}) = \underset{(0.712)}{3.6301} + \underset{(0.054)}{0.0842}\mathbf{DBH} - \underset{(0.017)}{0.02195}\mathbf{LCR} - \underset{(0.0007)}{0.0028}\mathbf{TPA} + \underset{(0.005)}{0.0270}\mathbf{DBH.perc} + \underset{(0.001)}{0.0025}\mathbf{DBH{:}LCR} - \underset{(0.0004)}{0.0012}\,\mathbf{DBH{:}DBH.perc}$$

where TC is dead branch biomass in pounds. This model's back-transformed pseudo-R-squared was 0.91, its RMSE was 88.31dry lbs, and its MAE was 58.34 dry lbs (16.4% of total crown biomass). The equation slightly under predicts, with a mean bias of -9.71 lbs. Unlike the live crown model, transformations of predictor variables did not improve performance. *Figure 7* illustrates model performance and comparison of predicted and observed total (live and dead) crown values for the modeling dataset (FR and UW). Standard errors are reported beneath each coefficient.

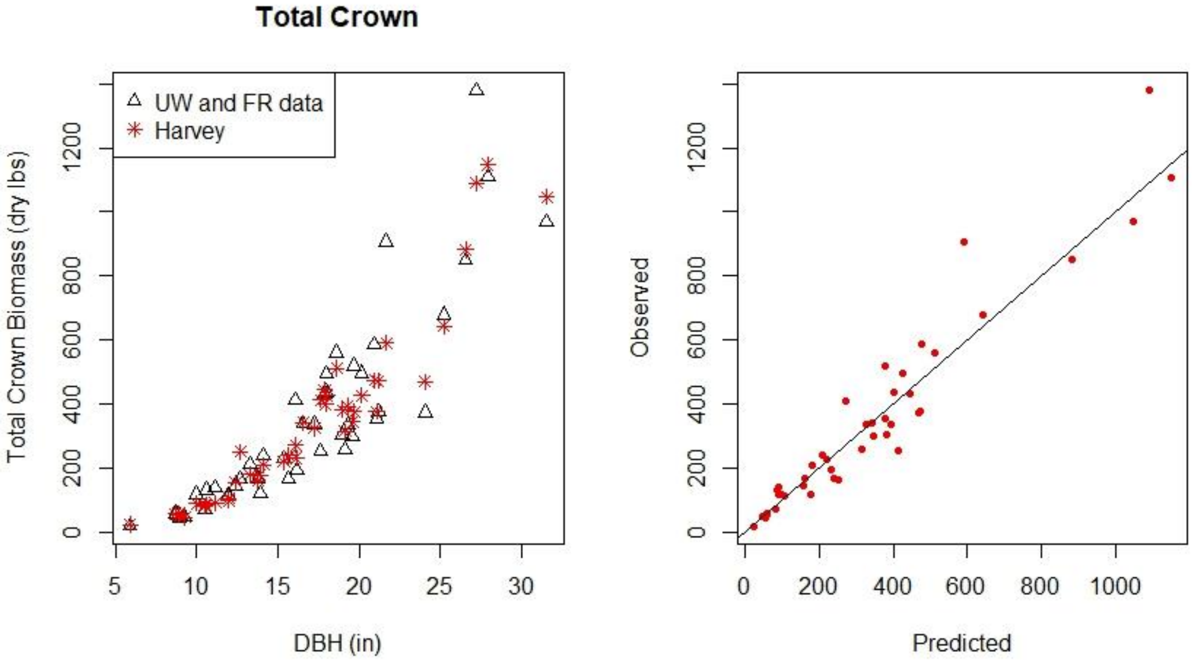

Figure 7) Predictions for total live and dead crown biomass (dark red) against observed values from the FR and UW trees

Table 3) Model performance metrics for the component biomass equations developed in this study when applied to their own training data set, UW and FR trees.

Model Performance on Training dataset (UW + FR)

Model	MAE (dry lbs)	MAE as Percent	RMSE (dry lbs)	Pseudo R2	Bias
[1] Total Live Crown	52.6	21.10%	78.5	0.856	-6.5
[2] Live Branches	43.2	21.90%	62.1	0.877	-1.7
[3] Foliage	14.7	27.90%	23.4	0.568	-0.4
[4] Dead Branches	35.6	33.70%	53.9	0.691	-7.6
[5] Total Crown	58.3	16.40%	88.3	0.911	-9.7

3.6 MODEL VALIDATION

Although the differences between the modeling data (FR and UW) and validation data set might seem substantial, the exclusively diameter-based biomass equations generated by the SISK study actually fit the FR and UW data moderately well and the mean live-branch-biomass/DBH ratio of the two datasets were similar ([UW + FR]: 10.08 lbs/in , SISK: 10.68 lbs/in). These two facts combined suggest that the use of the SISK data for model validation is acceptable, and thus allow a very rare measure of model assessment in the world of biomass modeling; assessment of model performance on a completely independent dataset. The SISK data do not include measurements for dead branches, so models for total crown and dead branch biomass could not be tested. Of the three models examined, the total live crown model (*Figure 8*) performed best with an MAE of 16.6% (of mean total live crown biomass). The live branch model (*Figure 9*) produced an MAE of 30.3% (of mean branch biomass), and the foliage model (*Figure 10*) yielded an MAE of 27.9% (of mean foliage biomass) when benchmarked with the SISK data. Model validation performance metrics are summarized in *Table 5*. No dramatic residual patterns were produced by any of the three component predictions. Neither the live branch model nor the foliage model out-performed their DBH-based counterparts developed by Nay and Bormann (live branch MAE: 21.06% and foliar MAE of 23.08%).

Table 4) Model performance metrics for the component biomass equations developed in this study when applied to the fully-independent SISK validation data set

Model performance on validation dataset (SISK)					
Model	MAE (dry lbs)	MAE as Percent	RMSE (dry lbs)	Pseudo R2	Bias
[1] Total Live Crown	43.1	16.60%	74.4	0.906	-15.6
[2] Live Branches	67.2	30.30%	89.1	0.776	-42.9
[3] Foliage	27.3	27.90%	38.4	0.663	-17.99

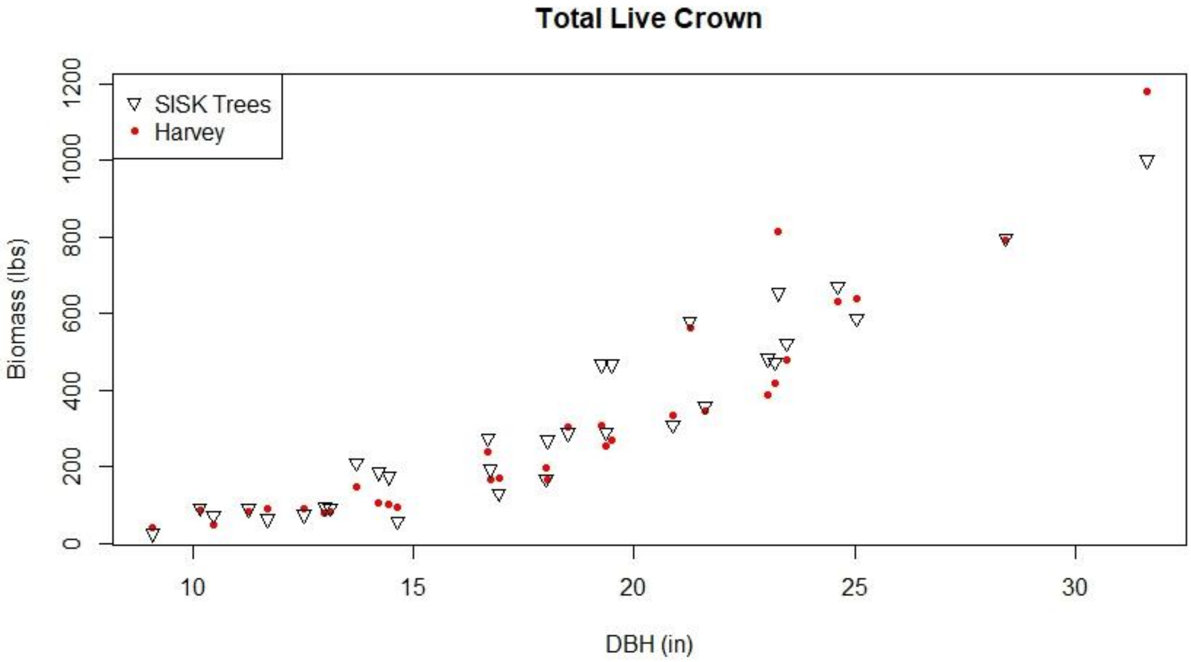

Figure 8) Predictions for total live crown biomass of SISK trees using equation [1] (red) against observed SISK values. It is important to mention again that the SISK data was not used in model construction.

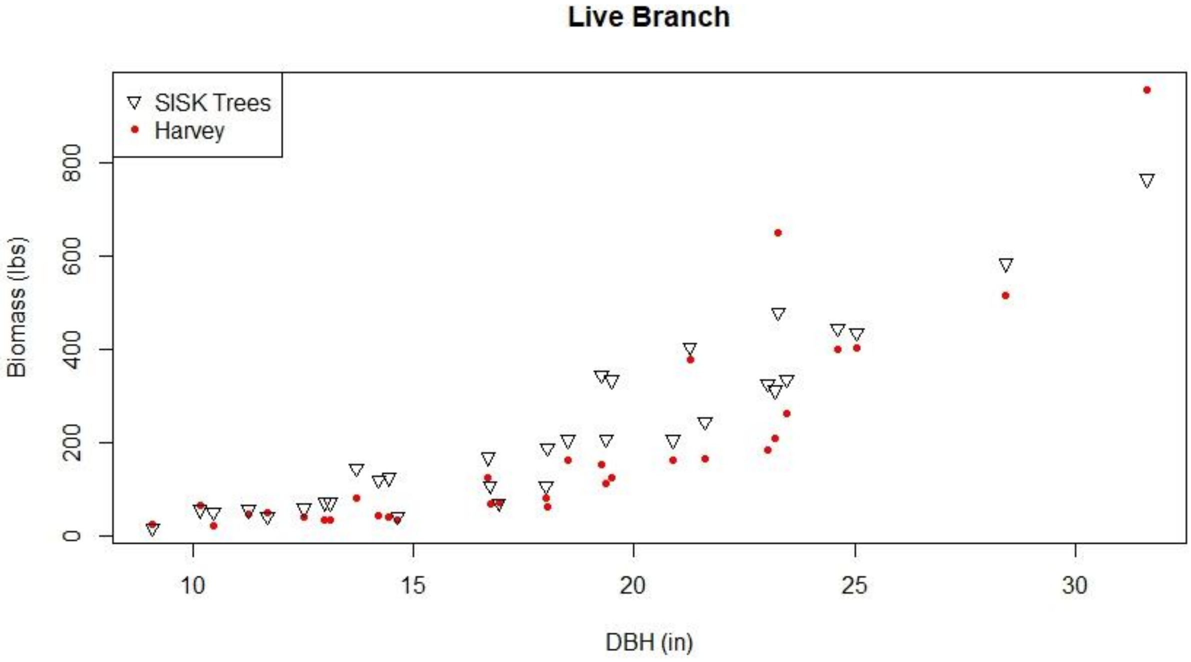

Figure 9) Predictions for total live branch biomass of SISK trees using equation [2] (red) against observed SISK values.

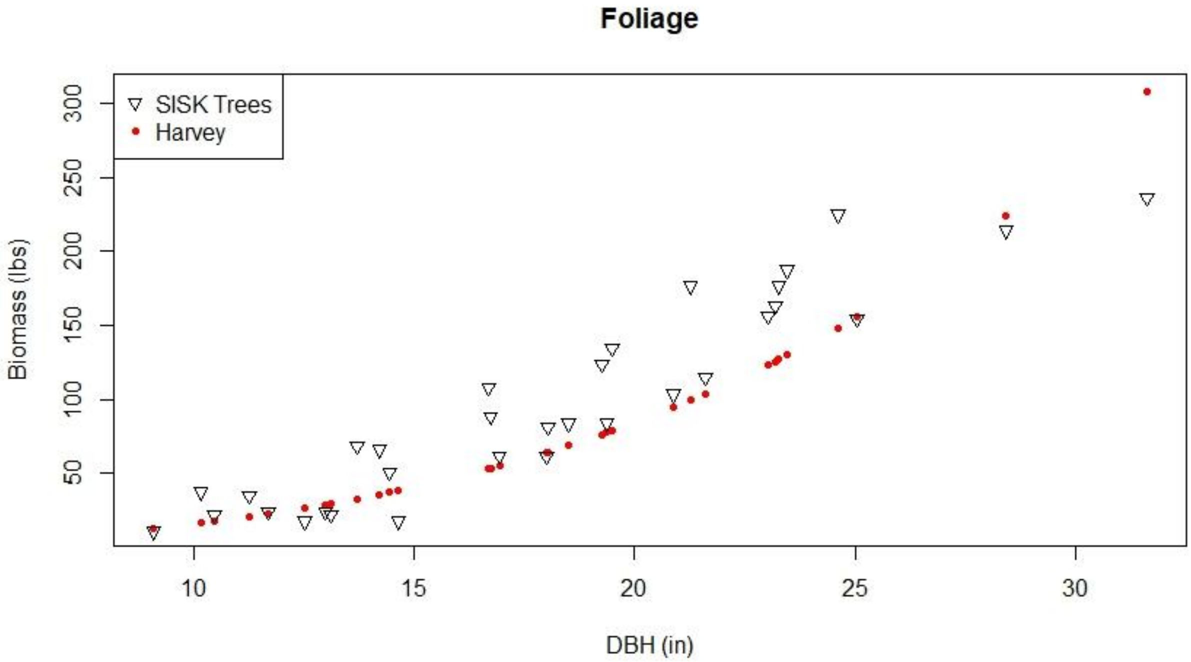

Figure 10) Predictions for total foliar biomass of SISK trees using equation [3] (red) against observed SISK values. Note that variation in predictions as a result of differences in BAA and RD are not visible here, as the SISK trees all come from the same stand.

3.7 MODEL COMPARISON

Model performance (for models [2] and [3]) was also compared to predictions generated using Gholz's (1979) regionally specific biomass equations as well as the models that Nay and Bormann (2014) developed, both of which estimate Douglas-fir component biomass using only DBH. *Figures 11 and 12* illustrate these comparisons when applied to the original modeling data (combined UW and FR). The Gholz equations proved slightly more effective than the Nay models with a live branch MAE of 27.6% and a foliar biomass MAE of 58.7%. The Nay equations yielded a Live branch MAE of 29.7% and a foliage MAE of 66.8%. Both models under predicted branch biomass and over predicted foliage biomass when applied to the FR and UW trees. Neither sets of equations outperformed their counterparts produced by this study (models [2] and [3]). Only these two component estimates were assessed to give the other methods the most fair comparisons as possible, given that neither Gholz nor Nay and Bormann developed a standalone live crown model and numerous authors describe issues related to summing predictions generated by component-specific equations (e.g., Chiyenda and Kozak 1984, Cunia and Briggs 1985, Car-valho and Parresol 2003).

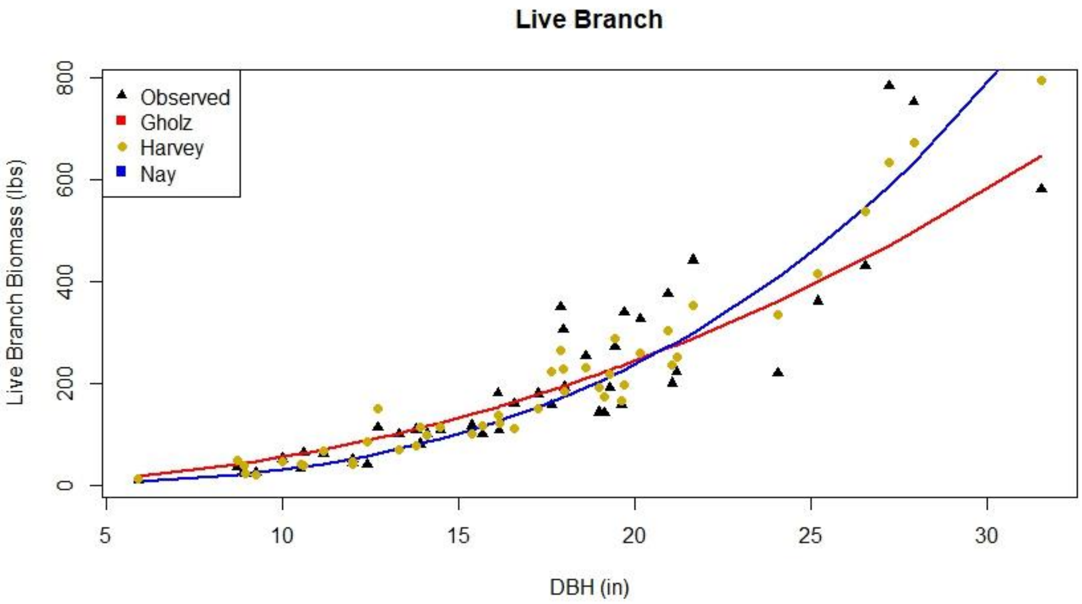

Figure 11) Comparison of live branch biomass predictions from Gholz, Nay and Harvey (model [2]) when applied to the modeling data set used for this study (FR and UW trees)

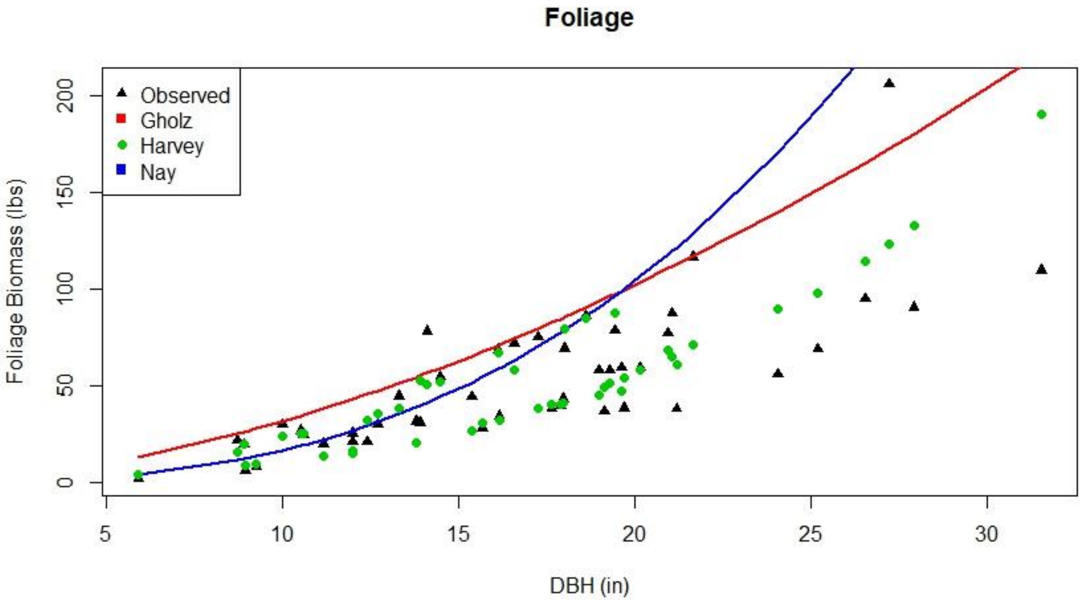

Figure 12) Comparison of foliar biomass predictions from Gholz, Nay and Harvey (model [3]) when applied to the modeling data set used for this study (FR and UW trees)

DISCUSSION

A variety of factors could contribute to the differences in behavior between the models examined in this study. Both the Nay and Gholz models performed particularly poorly when predicting foliage of the FR and UW trees. For the Nay foliage model, this phenomena would make sense for a number of reasons given the vastly different sampling location, stand conditions and sampling techniques. It is curious, however, that the Nay model consistently over-predicts foliage. If the issues were related to sampling technique, one would think that the Nay models would under-predict foliage, since the data for the FR and UW studies was generated through weighing the entire crown, while the SISK foliage data was modeled by branch diameter. It is possible that modeling total tree foliage through branch diameters somehow inflates results, but additional research would be needed to fully explore this issue. However, the fact that the Gholz equations also over-estimate foliage suggests that there may be another cause, since the trees used for that analysis were also fully destructively sampled. Other possibilities could be latitude, or misrepresentative sampling. The Gholz analysis uses 107 destructively sampled Douglas-fir trees, 80 of which are from Washington State. This would indicate a high level of applicability to the UW and FR trees, if not for the fact that that all 80 of Gholz's Washington samples are almost as small, or smaller, than the minimum sized trees of the UW and FR data. All 80 of Gholz's Washington trees are between 0.7-inches and 9-inches, while only the four smallest UW and FR trees are under 9-inches. Furthermore, of the 27 Gholz trees sampled in Oregon, only about ten fall within the range of diameters seen in the UW and FR dataset. In summary, although the Gholz equations were developed with a large dataset, only about 15 of those 107 trees are of suitable size to successfully apply to the modeling data used in this report, and majority of those 15 trees are from Oregon.

Even though the equations produced in this analysis did not outperform their site-specific DBH-based counterparts when estimating component biomass of the SISK trees, the level of error is impressively small given how vastly different the SISK site is. Furthermore, the fact that the models produced by Nay and Bormann exhibited large errors (particularly when predicting foliage) when applied to the FR and UW data suggests that they are study-specific and not necessarily applicable to stands in Washington State, industrial stands, or perhaps even stands at lower elevations. However, it should be noted that the authors acknowledge and address this possibility in their report, and should be applauded for publishing their dataset with the intent of assisting the progress of Douglas-fir research.

The fact that the models reported in this analysis demonstrate some level of predictive ability on naturally regenerated, mixed-age Douglas-fir, even though the model training data consists exclusively of planted industrially-managed trees, is highly intriguing. Additional naturally regenerated validation data would be needed to sufficiently explore and test specific model coefficients, but at the very least, this analysis highlights the role that certain stand measurements could play in modeling biomass (particularly RD, TPA and BAA). Other research indicates that latitude can have an influence on crown form (Hann 1997, Reich et. al. 1996) and thus could also play a role in augmenting biomass models. Although it was not included in any of the final models, there were some term combinations where latitude was a significant addition. There is also a possible indication of latitude influence in the fact that the validated models ([1], [2] and [3]) all demonstrated relatively large negative bias when applied to the SISK dataset, which is further south than any of the FR or UW plots. Having said that, this phenomena could also be an effect of elevation given that the SISK plot is also much higher in elevation than the majority of the UW and FR trees. Additional validation data or incorporation of the SISK dataset coupled with cross-validation could be useful for exploring these effects.

CONCLUSIONS

This work demonstrates the possibility of incorporating stand conditions into generalized component biomass models in order to successfully estimate coastal Douglas-fir crown biomass components, but as with any research, more questions have been raised and much more work is on the horizon. Extending analysis of the UW dataset will allow the examination of these variables' influence on bark and bole characteristics and use of the older cohort of UW trees will help us to better understand effects of latitude, elevation and stand age on the crown components examined in this study.

Furthermore, the models reported here were merely the best predictive equations for each respective crown component, but are not necessarily the most useful for other researchers or land managers. Height measurements are often difficult to quickly obtain in dense stands with precise accuracy and are often not an element of an industrial-style inventory. Therefore, it could be more beneficial to re-fit models that only include DBH and diameter-based stand metrics (such as BAL, BAA, QMD.ratio) along with broad, easy-to-measure environmental measures (latitude, elevation, stand age).

Another excellent application for the data used in this study that was not expressly accounted for, is to better inform remote-sensing-based forest measurements. One of the great strengths of LiDAR, areal imagery and other forms of remotely-sensed data, is to describe a tree's crown characteristics, while canopy penetration to examine tree stems and stem-related stand metrics is still a limitation for even the most advanced techniques (Richardson and Moskal, 2011). Since the results of this research demonstrate the possibility of using stand metrics to help predict tree crown components, it seems reasonable that a researcher could work backwards, and use the detailed crown attributes measured in this study with their corresponding stand metrics, to draw a clearer connection between tree characteristics that can be easily measured by remotely sensed data (height, crown mass, crown volume) and correlated stand attributes (BAA, RD, TPA).

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